



SEQUENCE LISTING

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LONNROTH, Christina

<120> ANTISECRETORY FACTOR PEPTIDES REGULATING PATHOLOGICAL
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<130> 003300-467

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<141> 1998-03-13

<150> PCT/SE96/01049

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<150> SE 9502936-9

<151> 1995-08-24

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<170> PatentIn Ver. 2.0

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<212> DNA

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr

atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat 155
Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
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gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac 203

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aac	gtg	ggc	ctt	atc	aca	ctg	gct	aat	gac	tgt	gaa	gtg	ctg	acc	aca	251	
Asn	Val	Gly	Leu	Ile	Thr	Leu	Ala	Asn	Asp	Cys	Glu	Val	Leu	Thr	Thr		
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ctc	acc	cca	gac	act	ggc	cgt	atc	ctg	tcc	aag	cta	cat	act	gtc	caa	299	
Leu	Thr	Pro	Asp	Thr	Gly	Arg	Ile	Leu	Ser	Lys	Leu	His	Thr	Val	Gln		
		65				70					75						
ccc	aag	ggc	aag	atc	acc	ttc	tgc	acg	ggc	atc	cgc	gtg	gcc	cat	ctg	347	
Pro	Lys	Gly	Lys	Ile	Thr	Phe	Cys	Thr	Gly	Ile	Arg	Val	Ala	His	Leu		
	80				85					90					95		
gct	ctg	aag	cac	cga	caa	ggc	aag	aat	cac	aag	atg	cgc	atc	att	gcc	395	
Ala	Leu	Lys	His	Arg	Gln	Gly	Lys	Asn	His	Lys	Met	Arg	Ile	Ile	Ala		
				100					105					110			
ttt	gtg	gga	agc	cca	gtg	gag	gac	aat	gag	aag	gat	ctg	gtg	aaa	ctg	443	
Phe	Val	Gly	Ser	Pro	Val	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Val	Lys	Leu		
			115					120					125				
gct	aaa	cgc	ctc	aag	aag	gag	aaa	gta	aat	gtt	gac	att	atc	aat	ttt	491	
Ala	Lys	Arg	Leu	Lys	Lys	Glu	Lys	Val	Asn	Val	Asp	Ile	Ile	Asn	Phe		
		130					135					140					
ggg	gaa	gag	gag	gtg	aac	aca	gaa	aag	ctg	aca	gcc	ttt	gta	aac	acg	539	
Gly	Glu	Glu	Glu	Val	Asn	Thr	Glu	Lys	Leu	Thr	Ala	Phe	Val	Asn	Thr		
	145					150					155						
ttg	aat	ggc	aaa	gat	gga	acc	ggt	tct	cat	ctg	gtg	aca	gtg	cct	cct	587	
Leu	Asn	Gly	Lys	Asp	Gly	Thr	Gly	Ser	His	Leu	Val	Thr	Val	Pro	Pro		
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ggg	ccc	agt	ttg	gct	gat	gct	ctc	atc	agt	tct	ccg	att	ttg	gct	ggt	635	
Gly	Pro	Ser	Leu	Ala	Asp	Ala	Leu	Ile	Ser	Ser	Pro	Ile	Leu	Ala	Gly		
				180					185					190			
gaa	ggt	ggt	gcc	atg	ctg	ggt	ctt	ggt	gcc	agt	gac	ttt	gaa	ttt	gga	683	
Glu	Gly	Gly	Ala	Met	Leu	Gly	Leu	Gly	Ala	Ser	Asp	Phe	Glu	Phe	Gly		
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gta	gat	ccc	agt	gct	gat	cct	gag	ctg	gcc	ttg	gcc	ctt	cgt	gta	tct	731	
Val	Asp	Pro	Ser	Ala	Asp	Pro	Glu	Leu	Ala	Leu	Ala	Leu	Arg	Val	Ser		
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gct	tct	gct	gct	gag	gcc	ggg	att	gct	acg	act	ggg	act	gaa	gac	tca	827	
Ala	Ser	Ala	Ala	Glu	Ala	Gly	Ile	Ala	Thr	Thr	Gly	Thr	Glu	Asp	Ser		
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 Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg
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act ggg ctt cct gac cta agc agt atg act gag gaa gag cag att gct 923
 Thr Gly Leu Pro Asp Leu Ser Ser Met Thr Glu Glu Glu Gln Ile Ala
 275 280 285

tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa 971
 Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu
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tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc 1019
 Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala
 305 310 315

aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag 1067
 Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln
 320 325 330 335

agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att 1115
 Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile
 340 345 350

cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga 1163
 Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
 355 360 365

agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg 1208
 Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
 370 375 380

tagctgagtc tgcttagggg actgcatggg aagcacggaa tatagggtta gatgtgtgtt 1268

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 35 40 45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
 50 55 60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65 70 75 80
 Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
 85 90 95
 Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
 100 105 110
 Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
 115 120 125
 Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
 130 135 140
 Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
 145 150 155 160
 Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
 165 170 175
 Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
 180 185 190
 Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
 195 200 205
 Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
 210 215 220
 Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
 225 230 235 240
 Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
 245 250 255
 Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
 260 265 270
 Gly Leu Pro Asp Leu Ser Ser Met Thr Glu Glu Glu Gln Ile Ala Tyr
 275 280 285
 Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
 290 295 300
 Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
 305 310 315 320
 Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
 325 330 335
 Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
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 Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg

355

360

365

Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
370 375 380